

Result No.	Query Match %	Score	Length	DB	ID	Description
1	97.3	4777.5	906	4	Q9UN21	homo sapien
2	88.4	4341.5	896	6	Q9GKL7	sus scrofa
3	87.5	4298	895	6	Q9GKN9	sus scrofa
4	77.8	3822.5	730	4	Q13771	homo sapien
5	58.5	2873	544	4	Q9BZG7	homo sapien
6	58.2	2857	542	4	Q9BZG6	homo sapien
7	57.9	2846.5	539	4	Q9NDA2	homo sapien
8	57.1	2802.5	531	4	Q9BZG5	homo sapien
9	49.2	2414.5	790	13	P70048	xenopus lae
10	34.1	1676	344	13	Q91445	serinus can
11	33.4	1639.5	853	13	Q93245	oncorhynch
12	33.2	1632.5	839	13	Q8GFV2	carassius a
13	32.7	1604	303	6	Q97684	ovis aries
14	32.7	1604	769	13	Q93497	pagrus major
15	31.6	1500	797	13	Q9PWG5	anguilla ja
16	31.7	1556	854	13	Q93244	oncorhynch

AC Q13771;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Androgen receptor.
GN AR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=90258935; PubMed=2342476;
RA Govindan M.V.;
RT "Specific region in hormone binding domain is essential for hormone
binding and trans-activation by human androgen receptor.";
RL Mol. Endocrinol. 4:417-427(1990).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; M73069; AAA51735.1; -;
DR HSP; P06536; IGDC.
DR InterPro; IPR001103; Andrgn_receptor.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; Znf_C4steroid.
DR Pfam; PF02166; Androgen_rec; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR ProDom; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLII; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 730 AA; 79150 MW; 918847C3B41B80C9 CRC64;

Query Match 77.8%; Score 3822.5; DB 4; Length 730;
Best Local Similarity 97.7%; Pred. No. 3.7e-256;
Matches 721; Conservative 0; Mismatches 2; Indels 15; Gaps 2;
QY 193 MQLLQQQQQAVSESSSGRRAREASGAPTSKDNLYGGTSTSDNAKELCKAVSVSMGLG 252
DB 1 MQLLQQQQQAVSESSSGRRAREASGAPTSKDNLYGGTSTSDNAKELCKAVSVSMGLG 60
QY 253 VEALHLSPEQLRGDCMAYPLIGVPAVRPTPCAPLAECKSLDDSDAGKSTEDTAEYS 312
DB 61 VEALHLSPEQLRGDCMAYPLIGVPAVRPTPCAPLAECKSLDDSDAGKSTEDTAEYS 120
QY 313 PFKGGYTKLGESLGCSSAAGSSGTLPLSTLSLYKSGALDRAAYQSRDYNFPLA 372
DB 121 PFKGGYTKLGESLGCSSAAGSSGTLPLSTLSLYKSGALDRAAYQSRDYNFPLA 180
QY 373 LAGPPPPPPPHPHARIKLENPLDYGSAWAAAACRYGDLASLHGAAGPGSGPSAA 432
DB 181 LAGPPPPPPPHPHARIKLENPLDYGSAWAAAACRYGDLASLHGAAGPGSGPSAA 240
QY 433 ASSSWHTLFTAERGQLYGPCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 492
DB 241 ASSSWHTLFTAERGQLYGPC-----GGGGGGGGGGGGGGGGGGGGGGGGGG 292
QY 493 LAGQESDFTAPDWWYGGMVSRVPYPTCVKSEMGPMWDSYSGPYGDMRLTARDHVL 552
DB 293 LAGQESDFTAPDWWYGGMVSRVPYPTCVKSEMGPMWDSYSGPYGDMRLTARDHVL 352
QY 553 IDYFFPQKTLICGDEASGCHYGALTCGSKVFFKRAEAGKQKYLCAASRNDCTDKFRR 612
DB 353 IDYFFPQKTLICGDEASGCHYGALTCGSKVFFKRAEAGKQKYLCAASRNDCTDKFRR 412
QY 613 KNCPSRLRKCYEAGMTLGARKLKKLGNLKLQEGEASSTTSPTETTKLTVSHIEGYE 672
DB 413 KNCPSRLRKCYEAGMTLGARKLKKLGNLKLQEGEASSTTSPTETTKLTVSHIEGYE 472

QY 673 COPIFLNVLEAIEPGVVCAGHDNNQPDFAALLSSLNELGRELQVLHVVKWAKALPGFRNL 732
DB 473 COPIFLNVLEAIEPGVVCAGHDNNQPDFAALLSSLNELGRELQVLHVVKWAKALPGFRNL 532
QY 733 HVDDQMAVIOYSWGLAVFANGWRSFTNVNSRMILYFAPDLVFNFRMHKSRMSYQCYRMR 792
DB 533 HVDDQMAVIOYSWGLAVFANGWRSFTNVNSRMILYFAPDLVFNFRMHKSRMSYQCYRMR 592
QY 793 HLSQEFGLQITPQOEFLLCMKA-----LLLSFIIPVDGLKNQKFFDELRMNYIKELDRI 845
DB 593 HLSQEFGLQITPQOEFLLCMKAMLIFFFLLSFIIPVDGLKNQKFFDELRMNYIKELDRI 652
QY 846 IACKRKNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEIIISV 905
DB 653 IACKRKNPTSCSRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDPEMMAEIIISV 712
QY 906 QVPKILSKGVPIYFHTQ 923
DB 713 QVPKILSKGVPIYFHTQ 730
RESULT 5
Q9BZG7 PRELIMINARY; PRT; 544 AA.
ID Q9BZG7
AC Q9BZG7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Androgen receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Megklara A., Diamandis E.P.;
RT "poly-Q and poly-G repeats in the androgen receptor of the breast
cancer cell line ZR-75-1.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321914; AAK09423.1; -;
DR InterPro; IPR001103; Andrgn_receptor.
DR Pfam; PF02166; Androgen_recep; 1.
DR Receptor.
KW NON_TER 544 544
FT NON_TER
SQ SEQUENCE 544 AA; 56013 MW; C97133EB6C922E74 CRC64;
Query Match 58.5%; Score 2873; DB 4; Length 544;
Best Local Similarity 99.6%; Pred. No. 1.3e-190;
Matches 542; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASILL--Q 58
DB 1 MEVOLGLGRVYPRPPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASILLQQQ 60
QY 59 QQQ 118
DB 61 QQQ 120
QY 119 SOPSALCEHPERCVCPEPAAVAASKGLPQOLPAPDEDDSAAPSTLSLGGTFFGLSS 178
DB 121 SOPSALCEHPERCVCPEPAAVAASKGLPQOLPAPDEDDSAAPSTLSLGGTFFGLSS 180
QY 179 CSADLKIDILSEATMQLQQQQQEAIVSESSSGRRAREASGAPTSKDNLYGGTSTSDNA 238
DB 181 CSADLKIDILSEATMQLQQQQQEAIVSESSSGRRAREASGAPTSKDNLYGGTSTSDNA 240
QY 239 KELCKAVSVSMGLGVEALEHLSPEQLRGDCMAYPLIGVPAVRPTPCAPLAECKSLDD 298
DB 241 KELCKAVSVSMGLGVEALEHLSPEQLRGDCMAYPLIGVPAVRPTPCAPLAECKSLDD 300
QY 299 DSAGKSTEDTAEYSPFKGGYTKLGESLGCSSAAGSSGTLPLSTLSLYKSGALDEA 358
DB 301 DSAGKSTEDTAEYSPFKGGYTKLGESLGCSSAAGSSGTLPLSTLSLYKSGALDEA 360

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QY 359 AAYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 418
|||||
Db 361 AAYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 420
|||||
QY 419 AGAAGPGSGSPSAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGA 478
|||||
Db 421 AGAAGPGSGSPSAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGA 480
|||||
QY 479 GAVAPGYTRPPQGLAQESDFTAPDVWYVPGMWVSRVYPSPTCVKSEMPWMDSYSGPY 538
|||||
Db 481 GAVAPGYTRPPQGLAQESDFTAPDVWYVPGMWVSRVYPSPTCVKSEMPWMDSYSGPY 540
|||||
QY 539 GDMR 542
|||||
Db 541 GDMR 544

RESULT 6
Q9BZG6 PRELIMINARY; PRT; 542 AA.
ID Q9BZG6;
AC Q9BZG6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Androgen receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
cancer cell line BT-474."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321916; AAK09425.1;
DR InterPro; IPR001103; Andrgn_receptor.
DR Pfam; PF02166; Androgen_recep; 1.
KW Receptor.
FT NON_TER 542 542
SQ SEQUENCE 542 AA; 53628 MW; C363EF841CAFF7739 CRC64;

Query Match 58.2%; Score 2857; DB 4; Length 542;
Best Local Similarity 99.6%; Pred. No. 1.6e-189;
Matches 541; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASLLLL-QQ 59
|||||
Db 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASLLLL-QQ 60
|||||
QY 60 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 119
|||||
Db 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
|||||
QY 120 QPSALECHPERGCVPEPGAASAKGLPQOLPAPPPEDDSDAAPSTLSLLGTFPGLSSC 179
|||||
Db 121 QPSALECHPERGCVPEPGAASAKGLPQOLPAPPPEDDSDAAPSTLSLLGTFPGLSSC 180
|||||
QY 180 SADLKDILSEASTMQLLQOQQQEAQVSGSSGRAREASGAPTSKKNYLGSTISDNK 239
|||||
Db 181 SADLKDILSEASTMQLLQOQQQEAQVSGSSGRAREASGAPTSKKNYLGSTISDNK 240
|||||
QY 240 ELCKAVSVSMGLVGEALEHLSPGELRGDCMYPALGVPVAVRTPCAPLAECKGSLDD 299
|||||
Db 241 ELCKAVSVSMGLVGEALEHLSPGELRGDCMYPALGVPVAVRTPCAPLAECKGSLDD 300
|||||
QY 300 SAGKSTEDTAESYSPFKGGYTKGLESGESLGCSSAAAGSSGTLEPSTLSLYKSGALDEAA 359
|||||
Db 301 SAGKSTEDTAESYSPFKGGYTKGLESGESLGCSSAAAGSSGTLEPSTLSLYKSGALDEAA 360
|||||
QY 360 AYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 419
|||||
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Db 361 AYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 420
|||||
QY 420 GAAGPGSGSPSAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGA 479
|||||
Db 421 GAAGPGSGSPSAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGA 479
|||||
QY 480 AVAPYGYTRPPQGLAQESDFTAPDVWYVPGMWVSRVYPSPTCVKSEMPWMDSYSGPY 539
|||||
Db 480 AVAPYGYTRPPQGLAQESDFTAPDVWYVPGMWVSRVYPSPTCVKSEMPWMDSYSGPY 539
|||||
QY 540 DMR 542
|||||
Db 540 DMR 542

RESULT 7
Q9NUA2 PRELIMINARY; PRT; 539 AA.
ID Q9NUA2;
AC Q9NUA2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Androgen receptor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
cancer cell line T-47D."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF321915; AAK09424.1;
DR InterPro; IPR001103; Andrgn_receptor.
DR Pfam; PF02166; Androgen_recep; 1.
KW Receptor.
FT NON_TER 539 539
SQ SEQUENCE 539 AA; 55444 MW; AB493953B89D869F CRC64;

Query Match 57.9%; Score 2846.5; DB 4; Length 539;
Best Local Similarity 99.4%; Pred. No. 8.7e-189;
Matches 539; Conservative 0; Mismatches 0; Indels 3; Gaps 2;

QY 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASLLLL-QQ 60
|||||
Db 1 MEVOLGLGRVYPRPSKTYRGAFONLFQSVREVIONPGRHPEAASAPPGASLLLL-Q 58
|||||
QY 61 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 120
|||||
Db 59 QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 118
|||||
QY 121 POSALECHPERGCVPEPGAASAKGLPQOLPAPPPEDDSDAAPSTLSLLGTFPGLSSC 180
|||||
Db 119 POSALECHPERGCVPEPGAASAKGLPQOLPAPPPEDDSDAAPSTLSLLGTFPGLSSC 178
|||||
QY 181 ADLKDILSEASTMQLLQOQQQEAQVSGSSGRAREASGAPTSKKNYLGSTISDNK 240
|||||
Db 179 ADLKDILSEASTMQLLQOQQQEAQVSGSSGRAREASGAPTSKKNYLGSTISDNK 238
|||||
QY 241 LCKAVSVSMGLVGEALEHLSPGELRGDCMYPALGVPVAVRTPCAPLAECKGSLDD 300
|||||
Db 239 LCKAVSVSMGLVGEALEHLSPGELRGDCMYPALGVPVAVRTPCAPLAECKGSLDD 298
|||||
QY 301 SAGKSTEDTAESYSPFKGGYTKGLESGESLGCSSAAAGSSGTLEPSTLSLYKSGALDEAA 360
|||||
Db 299 SAGKSTEDTAESYSPFKGGYTKGLESGESLGCSSAAAGSSGTLEPSTLSLYKSGALDEAA 358
|||||
QY 361 AYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 420
|||||
Db 359 AYQSDYYNFPALAGPPPPPPPPHARIKLENPLDYGSAWAAAAAQCRCYGDILASLHG 418
|||||
QY 421 AAGPGSGSPSAASSSWHTLFTAEGLYGCPCGGGGGGGGGGGGGGGGGGGGA 480
|||||
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Db 419 AAGPGSGSAAASSWHTLFTAEGLYGPC-GGGGGGGGGGGGGGGGGGGGGEAGA 477
QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPPSPCTVKSEMGPMWDSYSGPYGD 540
Db 478 VAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPPSPCTVKSEMGPMWDSYSGPYGD 537
QY 541 MR 542
Db 538 MR 539

RESULT 8
ID Q9BZG5 PRELIMINARY; PRT; 531 AA.
AC Q9BZG5;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
DE Androgen receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Magklara A., Diamandis E.P.;
RT "Poly-Q and poly-G repeats in the androgen receptor of the breast
RT cancer cell line MCF-7."
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321917; AAK09426.1;
DR InterPro: IPR001103; Andrgn_receptor.
DR Pfam: PF02166; Androgen_recip; 1.
DR KW Receptor.
DR NON_TER 531
FT SEQUENCE 531 AA; 54419 MW; FA0D3AA60AC20DAB CRC64;

Query Match 57.1%; Score 2802.5; DB 4; Length 531;
Best Local Similarity 98.0%; Pred. No. 9.5e-186;
Matches 531; Conservative 0; Mismatches 0; Indels 11; Gaps 2;

QY 1 MEVQLGLGRVYPPPSKTYRGAFONLFQSVREVIONPGRHPEAASAAPGASLLLLQOQ 60
Db 1 MEVQLGLGRVYPPPSKTYRGAFONLFQSVREVIONPGRHPEAASAAPGASLLLL --- 57
QY 61 QQQQQQQQQQQQQQQQQQQQQTSRQ0000GGEDGSPQAHRRGPTGYLVLDEEQPSQ 120
Db 58 -----QQQQQQQQQQQQQQQQTSRQ0000GGEDGSPQAHRRGPTGYLVLDEEQPSQ 110
QY 121 POSALECHPERGCVPEPAAVASKGLPOOLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 180
Db 111 POSALECHPERGCVPEPAAVASKGLPOOLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 170
QY 181 ADLKDILSEASTMOLLQOQQQEAUSVSSSGSRRAREASGAPTSSKDNKLGSTISDNAKE 240
Db 171 ADLKDILSEASTMOLLQOQQQEAUSVSSSGSRRAREASGAPTSSKDNKLGSTISDNAKE 230
QY 241 LKAVSVNGLGVAELEHLSPEQLRGDCMYAPILGVPPAVRPTPCAPLAECKGSLDDSD 300
Db 231 LKAVSVNGLGVAELEHLSPEQLRGDCMYAPILGVPPAVRPTPCAPLAECKGSLDDSD 290
QY 301 AGKSTEDTAEYSPFKGGYTKLEGESLGCSSAAGSGSTLELPSTLSLYKSGALDEAAA 360
Db 291 AGKSTEDTAEYSPFKGGYTKLEGESLGCSSAAGSGSTLELPSTLSLYKSGALDEAAA 350
QY 361 YQSRDYNNFLALAGPPPPPPPPHARIKLENPLDYSANAAAAQCRYGDLASLHGAG 420
Db 351 YQSRDYNNFLALAGPPPPPPPPHARIKLENPLDYSANAAAAQCRYGDLASLHGAG 410
QY 421 AAGPGSGSAAASSWHTLFTAEGLYGPCGGGGGGGGGGGGGGGGGGGGEAGA 480
Db 411 AAGPGSGSAAASSWHTLFTAEGLYGPC-GGGGGGGGGGGGGGGGGGGGGEAGA 469

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QY 481 VAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPPSPCTVKSEMGPMWDSYSGPYGD 540
Db 470 VAPYGYTRPPQGLAGQESDFTAPDVWYPGGMVSRVPPSPCTVKSEMGPMWDSYSGPYGD 529
QY 541 MR 542
Db 530 MR 531

RESULT 9
P70048
ID P70048 PRELIMINARY; PRT; 790 AA.
AC P70048;
DT 01-FEB-1997 (T-EMBLrel. 02, Created)
DT 01-JAN-1999 (T-EMBLrel. 09, Last sequence update)
DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
DE Androgen receptor alpha isoform.
GN XL ALPHA AR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Fischer L., Catz D., Kelley D.;
RT "An androgen receptor mRNA isoform associated with hormone-induced
RT cell proliferation."
RL Proc. Natl. Acad. Sci. U.S.A. 90:8254-8258(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Fischer L.M., Catz D., Kelley D.B.;
RT "Androgen-directed development of the Xenopus laevis larynx: control
RT of androgen receptor expression and tissue differentiation."
RL Dev. Biol. 170:115-126(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Kelley D.B., Kamenetz F.R., Kelley D.B., Badea T.C.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL: U67129; AAC97386.1;
DR HSPSP; P06536; IGDC.
DR InterPro: IPR001103; Andrgn_receptor.
DR InterPro: IPR000536; Hormone_rec_lig.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF02166; Androgen_recip; 1.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS; PR000047; STROIDFINGER.
DR PRODOM; PD000035; Znf_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; Znf_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
DR Zinc-finger.
SQ SEQUENCE 790 AA; 86973 MW; 9E7FC136CCCC3906 CRC64;

Query Match 49.2%; Score 2414.5; DB 13; Length 790;
Best Local Similarity 54.5%; Pred. No. 1.2e-158;
Matches 523; Conservative 65; Mismatches 162; Indels 209; Gaps 29;

QY 1 MEVQLGLGRVYPPPSKTYRGAFONLFQSVREVIONPGRHPEAASAAPGASLLLLQOQ 60
Db 1 MEVHIGLGGYKQPPCKMIRGAFENFLSREALQ--GERALEGSOAPAGWS----- 51
QY 61 QQQQQQQQQQQQQQQQQQQQQTSRQ0000GGEDGSPQAHRRGPTGYLVLDEEQPSQ 120
Db 52 -----EAPGTHRS-----EAPQDGT 68
QY 121 POSALECHPERGCVPEPAAVASKGLPOOLPAPDEDDSAAPSTLSLLGPTFFGLSSCS 180

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RT J. Biol. Chem. 274:5674-5680(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL: AB012096; BAA32785.1; -.
DR HSP: P06536; 1GDC.
DR InterPro: IPR001103; Andrgn_receptor.
DR InterPro: IPR000336; Hormone_rec_lig.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF02166; Androgen_recep; 1.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00047; STROIDFINGER.
DR ProDom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOL1; 1.
DR SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 853 AA; 95776 MW; 65EFF5FD3B36F4C4 CRC64;

Query Match 33.4%; Score 1639.5; DB 13; Length 853;
Best Local Similarity 38.4%; Pred. No. 5.6e-105;
Matches 386; Conservative 129; Mismatches 252; Indels 239; Gaps 30;

QY 1 MEVQLGLGVYPRPPKTYRGAFONLFQSVREVIONPGPRHPEAASAAPPGASLILLLOQ 60
DB 1 MEIPVGLGVCD-SPNIVFRGPFQNVFHNKATL-----PSNTIVTETLDFSSYSFMQNK 55

QY 61 QQQQQQQQQQQQQQQQQQQQQQQTSRQQQQQQQ-----EDGSPQAH-----RRGPTG 108
DB 56 HPWEMRQNSPRKETSSTARNSDIEVKEDDSISFRTLESARRIHFASKSTGNKGT 115

QY 109 YLVLDDEQOP-----SQPSALECHPERGCVPEPCAAGAAAGKGLPQQLPAPDEDDSA 162
DB 116 FSSVNELDYPNANGYSGRGPCLACNTKQCCO-----PAPPHCVLS 159

QY 163 PSTLSLGLPTFPGLSSGADLKDILSEASTMQLLQOQOQEAIVSEGSSGRAREAGAPTS 222
DB 160 PNSYARVA-----NSCT----- 176

QY 223 SKNYLGGTSTISDNKELKAVSVSMGLGVE--ALEHLS-----GEOLRGDCMYAP 273
DB 177 -----TISTARELCNAYSLSGLTDLNEMNDLGNVPNAPSANDQSGNLFQ- 225

QY 274 LLGVPPAVRTPCAPLAECKSLDDSAAGKSTEDTAETSPFKGYTKGLESGSCGSA 333
DB 226 -----VPLNCSGA-----EENVSIYEK-----CPSE 249

QY 334 AAGSSGTLPLPSTLSLYKSGALDE-----AAVOSRDYVNFPLALAGPPPPPP 382
DB 250 ---NARPLQSDTRVYKFKSPANDLLEAVATMEHLSSRHPSTGEQEFRLNKSDDPTSK- 305

QY 383 PHPHARIKLEPLDYGSAWAAAAOCRYGLASLHGA--GAAGPG----- 425
DB 306 -----ETENSL-----STRASASCHFDPLPAHLAHFSQTPDRISSHVIAHVCETG 354

QY 426 -----SGPSAAASSWITLFTAEQGLYPCGGGGGGGG 461
DB 355 ETMEDKYADYLOQQYSVKIKYEAISNEPAGTSMGSGYNGYNDNDNTQYGP----- 404

QY 462 GGGGGGGGGGGGGEAGAVA-PGYTRPQGLAGQESDFTAPDVWYPGGMVSRVPPSP 520
DB 405 ----RQGMNPSAGPDSGFCINPYEYER--GGGLVRRR--PTSQWYTPGMLGRMYPNS 457

QY 521 TCVKSEMPWMDSYSGPYGDMRLTARDHVLPIIDYFPPOKTCILICGDEASGCHYGALT 580
DB 458 PYLKNVGDWLDV---SYTDARFEGGRDHMPMEFFPPORTCLICADEASGCHYGALT 514

QY 581 GSKVFFKRAAGKQKYLCAARNDCITDKFRKNCPCRLKCKYEAGMTLGARKLKLGN 640
DB 515 GSKVFFKRAAGKQKYLCAARNDCITDKLRKNCPCRLKCKFEAGMTLGARKLKLIG 574

QY 641 LKQERGEASSTTSPTETOKL-TVSHIEG--YECQIFLNVLEAIEBPGVCAGHDNQ 697
DB 575 LKSPPE-----DLPTQGPPTDAIQCVSPQSLTFHSQLVFLNILESEIEPVNAGHDQ 628

QY 698 PDSFAALLSLNELGERQLVHVYKAKALPGFNLHVDDQMAVIOYSWMLMVFAMGWS 757
DB 629 PDSAAVLLTSLNELGERQLVHVYKAKGMPGFRNLHVDDQMTVIQHSWGVVFGWRS 688

QY 758 FTNVNSRLYFAPDLVFNEMHKSRYMSQCVRMHLSQEFGLQITPOEFLCMKALLF 817
DB 689 YKVNARMYFAPDLVFNDRHMLSSMFEHCIRMRHLSQGFVLLQVTOEFLCMKALLF 748

QY 818 SIIPVDGLKNKFFDELRMNYIKELORIIACKRNTPSCSRFYOLTKLLDSVOPTAREL 877
DB 749 SIIPVDGLKSKYFDELRLTYINELDRVINYGRK--SNCSQRFYQLTRMLDSLOPIVRKL 806

QY 878 HQFTFDLLIKSHMV--SVDPPEMMAETISVOYPKILSGKVKPIVFH 921
DB 807 QQFTFDLFIQAQSLPTKVSFPEMIAELISVHVPKILAGLAKPILFH 852

RESULT 12
Q8QFV2 PRELIMINARY; PRT; 839 AA.
AC Q8QFV2; Q8QFV2; 839 AA.
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Androgen receptor.
GN AR.
OC Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Betka M., Rothberg S.C., Callard G.V.;
RT "Carassius auratus Androgen receptor."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
KW EMBL; AY090897; AAM09278.1;
KW Receptor.
SQ SEQUENCE 839 AA; 93168 MW; A534DC3169C0B1F4 CRC64;

Query Match 33.2%; Score 1632.5; DB 13; Length 839;
Best Local Similarity 43.9%; Pred. No. 1.7e-104;
Matches 384; Conservative 103; Mismatches 225; Indels 163; Gaps 26;

QY 130 ERGCVPEPAA-----VAASKGLPQQLPAPPDEDDSAAPSTLSLLGPTFGLSSCSADL 183
DB 44 KRGCLQETDSTKRPKSLSPSKI---ICCPKKECESASSXMRSSIGSKSDTSLSCGRA 100

QY 184 KDILSEASTMQLLQ-----QQQEAIVSEGSSGRAREASGAPTSSKNDYLGCTSTISDNK 239
DB 101 DATSSGSRAGFLRGAESGOKSCATAEVHSRRDARVASSSRACNTTTSSSSSSISSETAR 160

QY 240 ELCKAVSVSMGLGVEALE-----HLSPGEOLRDCMYAPLLGVPPAVRTPCAPLAEC 292
DB 161 ELCKAVSVSLGLAMESSELGDVEPHVPPPLTTKSSERIYLFM-----PILNC 210

QY 293 KGLLDDSAKSTEDTA-----EYSPFKGYTKGLEGE--SLGCSGA- 333
DB 211 --SVSRXAGGKEREYALAAAGRDRAELRDRLLMEFKSGDLEQAGEVTLQCSSASR 268

QY 334 ---AAGSSGTLELPST-----LSLYKSGA---LDEAAVQSRDYVNFPLALA----- 374
DB 269 SHLTADAQGVHEFASVSGDIANLSSEGTTPDMDTFRASCOFEQLLPVSMAHFYQPELE 328

QY 375 -GPPPPPPPPHP-----HARIKLE-NPLDYGSAWA---AAACQ--RYG 411
DB 329 NGPNQSFAPKPAEMSGFEAGFVDEYVNLVNVKIAEMMPRELNDTWAPHRYAEDCNGQY 388


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QY 412 DLASLHAGACGPGSGPSAASSSWHLFTAEGLQYPCGGGGGGGGGGGGGGGGGG 471
Db 389 -----SPKQRTTYASHDT-HFICNPYE----- 410
QY 472 GGGGGAAGAVPYGYGTPOGLAGQESDFTAPDVWYPGMVSRVPYSPCTCVKSGEMGPM 531
Db 411 ---YGRNEALVP--RERP-----PEQWYPGMLTRPPYPMPCCKNMGNNWL 453
QY 532 DSYSPGYGDMRLTARDHVLFDYFPQKTCCLGDBASGCHYGALTCGSKCVFFKRAA 591
Db 454 DVTS--LTDGRFDGRSDIFPMEFFLPQRTCLICSDEASGCHYGALTCGSKCVFFKRAA 511
QY 592 EGKQYLCASRNDCTIDFRKNCPCSLRKYCAGMTLGARKLKLGNLKLQEGEASS 651
Db 512 EGKQYLCASRNDCTIDFRKNCPCSLRKYCAGMTLGARKLKLGNLKLQEGEASS 566
QY 652 TTSPT-----ETQKLTSHIEGYEQPIFLNVLAEIPGVVACAGHNNQDPSFAALLSSL 708
Db 567 -VGPVQSGSETIOCLSPKPSLTFHSQILFLNILESIEPEVVNAGHDHQAQDPSAVALLTSL 625
QY 709 NELGERQLVHVVKAKALPGFRLNHLVDQMAVIOYSWMGLMVFAMGWSRFTNVNSRMLYF 768
Db 626 NELGERQLVHVVKAKALPGFRLNHLVDQMTVIQHTWGMVVMFALGWSRYKNANARMLYF 685
QY 769 APDLVFNERYMHKSRMYSOCVYMRHLHLSOEFGLWQITPOEFLCMKALLFSIIPVDGLKNQ 828
Db 686 APDLVFNDRHMHISMYEHCVMQHLHLSOEFVLLQVTOEFLCMKALLFSIIPVEGLKQS 745
QY 829 KFFDELNMNLIKELDRIIACKRNKPTSCSRFFYOLTLLDSVQPIARELHOFTEFLLIKS 888
Db 746 KYFDDLRLTYINELDLRLNYSRK--TNCAMRFQQLTRMLDSIQPIVRKLHOFTEFLLVQA 803
QY 889 HMV--SVDFPEMMAEIIISVQVPKILSGKVKPIYFH 921
Db 804 RSLPTKVSFPEMAEIIISVQVPKILAGLSKPILFH 838

RESULT 13
O97684 PRELIMINARY; PRT; 303 AA.
AC O97684;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Androgen receptor (fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DORSET;
RA Thonney M.L., Ignatz G., Richards H.M.;
RT "Partial sequence of an ovine androgen receptor cDNA.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AF105713; AAC97958.1; -.
DR HSSP; P06536; 1GLU.
DR InterPro; IPR001723; Hormone_rec_lig.
DR InterPro; IPR001723; Strdhmn_receptor.
DR InterPro; IPR001628; ZnF_C4steroid.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00398; STRDHMONER.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; ZnF_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
FT NON_TER 1 1
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FT NON_TER 303 303
SQ SEQUENCE 303 AA; 34673 MW; D14D3950C7DC69D1 CRC64;

Query Match 32.7%; Score 1604; DB 6; Length 303;
Best Local Similarity 99.0%; Pred. No. 4e-103; 3; Indels 0; Gaps 0;
Matches 300; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 564 LICGDEASGCHYGALTCGSKCVFFKRAAGCKQKYLCAASRNDCTIDFRKNCPCSLRKC 623
Db 1 LICGDEASGCHYGALTCGSKCVFFKRAAGCKQKYLCAASRNDCTIDFRKNCPCSLRKC 60
QY 624 YEAGMTLGARKLKLGNLKLQEGEASSSTTSPTTEETQKLTVSHIEGYEQPIFLNVLAE 683
Db 61 YEAGMTLGARKLKLGNLKLQEGEASSSATSPTEPAQKLTVSHIEGYEQPIFLNVLAE 120
QY 684 IEPGVVACAGHNNQDPSFAALLSSLNELGERQLVHVVKAKALPGFRLNHLVDQMAVIOY 743
Db 121 IEPGVVACAGHNNQDPSFAALLSSLNELGERQLVHVVKAKALPGFRLNHLVDQMAVIOY 180
QY 744 SWMGLMVFAMGWSRFTNVNSRMLYFAPDLVFNERYMHKSRMYSOCVYMRHLHLSOEFGLWQI 803
Db 181 SWMGLMVFAMGWSRFTNVNSRMLYFAPDLVFNERYMHKSRMYSOCVYMRHLHLSOEFGLWQI 240
QY 804 TPOEFLCMKALLFSIIPVDGLKNQKFFDELNMNLIKELDRIIACKRNKPTSCSRFFYOL 863
Db 241 TPOEFLCMKALLFSIIPVDGLKNQKFFDELNMNLIKELDRIIACKRNKPTSCSRFFYOL 300
QY 864 TKL 866
Db 301 TKL 303

RESULT 14
O93497 PRELIMINARY; PRT; 769 AA.
AC O93497;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Androgen receptor.
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.
OX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99326178; PubMed=10395960;
RA Tsuchida K., Kinoshita M., Tokuda Y., Toyohara H., Sakaguchi M.,
RA Yokoyama Y., Yamashita S.;
RT "Sequence and expression of a cDNA encoding the red seabream androgen
RT receptor.";
RL Biochim. Biophys. Acta 1450:481-485(1999).
CC -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL; AB017158; BAA33451.1; -.
DR HSSP; P06536; 1RGD.
DR InterPro; IPR001103; Andrgn_receptor.
DR InterPro; IPR000536; Hormone_rec_lig.
DR InterPro; IPR001628; ZnF_C4steroid.
DR Pfam; PF02166; Androgen_recep; 1.
DR Pfam; PF00104; hormone_rec; 1.
DR Pfam; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
DR PRODOM; PD000035; ZnF_C4steroid; 1.
DR SMART; SM00430; HOLI; 1.
DR SMART; SM00399; ZnF_C4; 1.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
KW DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 769 AA; 86081 MW; 9305C627DBE42062 CRC64;
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Query Match      32.7%; Score 1604; DB 13; Length 769;
Best Local Similarity 43.9%; Pred. No. 1.4e-102;
Matches 363; Conservative 79; Mismatches 171; Indels 214; Gaps 23;

QY 205 SEGSSGRAREASGA-PTSSKDYL----- 228
DB 46 STNGAGRMREADNADNTYESGHMPLVCDMEKHCCQTAAAPQELFNADCRVGDERSF 105
QY 229 GGTSTISDNACKELKAVSYSMGLGVE-----ALEHLSPEQLRGDCMYAPLLGVPP 279
DB 106 SACATISARELCKAVSYSLGLAMESNDPSDMAALSQAANDQLRGYLFQ----- 158
QY 280 AVRPFCAPLAECKGLLDDSAKSTEDTAEYSPKGGYTKLEGSIGCSGSAAGSSG 339
DB 159 ---VGAAPLS-CPGA-----QAAYSEYKCPPEERLHGK----- 188
QY 340 TLEPSTLSLYKSGALDEAAAYQSR-----DYNFPLALAGPPPPPPHAPHARIKL 391
DB 189 ---QQQLMDMFKS---SETGAHLQHLSTRTVPDEHNFILCKAEDLTPEETAHQD----- 238
QY 392 ENPLDYGSAAWAAAAOCRYGDLASLHGAAGPGS-----GSPSAASSSWHTLFTAEGQ 447
DB 239 -----SVRAACAPY-----AQALPGNMAHFGSP--APERDW-----Q 269
QY 448 LYPCGGGGGGG-----GGGGGGGGG----- 469
DB 270 LYKPPDEAGDFGVMESRPVTSYQPEYSVKICBEDTESALMGNGTTFNDRVNSQW 329
QY 470 -----GGGGGGGAGAVAPYGYTRPPQGLAGQESDFTAPDVWYVPGMVSRYVPSPTCV 523
DB 330 GPRQCNNAHSTGANSALCHPY-----ERSVARPEHWYPCGML-RSPYFNSSVY 376
QY 524 KSEMGFWMDSYSGPYGDMRLFTARDHVLIDYFFPQKTYCLICGDBASCHYGALTCGSC 583
DB 377 KSEVGWLDV---PYSDPRFDSSEHMFMEFFPFAQRMCILCSDBASCHYGALTCGSC 433
QY 584 KVFFKRAAEKQYLCASRNDCTIDFRKNCPCSLRKYCAGMTLGARKLKLGNLK- 642
DB 434 KVFFKRAAEKQYLCASRNDCTIDLRKNCPCSLRKYCAGMTLGARKLKLGNLK- 493
QY 643 -----LOEGERASSTSTPEETQKLTSHIEGYEQPIFLNVLFAIEPVVCAAGHNN 696
DB 494 SDEHPLQEPAEVMPNTPSKGLS-----FNSQVVLNVLIESIEPVVNAHDYV 543
QY 697 QPDSFRAALLSINELGERQLVHVKKAKALPGRNLHVDQDMAVIOYSNGLMVFAMGR 756
DB 544 QPDSAAFTLTLSELGERQLVHVKKAKALPGRNLHVDQDMVIOHSNGLMVFAMGR 603
QY 757 SFTNVSRLMYPADLVFNEYRMHGRMYSQVYMRHLHSDQEWLQITPOEFLCMKALL 816
DB 604 SYKNVGRMLYFADLVFNEYRMHGRMYSQVYMRHLHSDQEWLQITPOEFLCMKALL 563
QY 817 FSIIPVDLKNQKFFDELRLNMYIKELDRITACKRKNTSCSRFVOLTLLKLDVQPIARE 876
DB 664 FSIIPVGLKSKQYFDELRLTYINELRLNMYINRMN--TNCQRFYQTLRLDLSQMTVK 721
QY 877 LHOFTFDLLIKSHW--SVDFPEMAEILSVQVPKILSGKVRPIYH 921
DB 722 LHOFTFDLVQASLPTKVSFPEMGEILSVHVPKILAGLAKPILFH 768

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RESULT 15
Q9PWG5 PRELIMINARY; PRT: 797 AA.
AC Q9PWG5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Androgen receptor-beta.
GN AK-BETA.
OS Anguilla japonica (Japanese eel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;

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OC Anguilla.
OX NCBI_TaxID=7937;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE=99395076; PubMed=10464240;
RA Ikeuchi T., Todo T., Kobayashi T., Nagahama Y.;
RT "cDNA cloning of a novel androgen receptor subtype.";
RL J. Biol. Chem. 274:25205-25205(1999).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
DR EMBL: AB025361; BAA83805.1;
DR HSSP: P06536; IGDC.
DR InterPro: IPR001103; Andrgn_receptor.
DR InterPro: IPR000536; Hormone_rec_lig.
DR InterPro: IPR001723; Stdhmn_receptor.
DR InterPro: IPR001628; Znf_C4steroid.
DR Pfam: PF00166; Androgen_recep; 1.
DR Pfam: PF00104; hormone_rec; 1.
DR Pfam: PF00105; zf-C4; 1.
DR PRINTS: PR00398; STRDHORMONER.
DR PRINTS: PR00047; STROIDFINGER.
DR PRODom: PD000035; Znf_C4steroid; 1.
DR SMART: SM00430; HOLI; 1.
DR SMART: SM00399; Znf_C4; 1.
DR PROSITE: PS00031; NUCLEAR_RECEPTOR; 1.
DR DNA-binding; Nuclear protein; Receptor; Transcription regulation;
KW Zinc-finger.
SQ SEQUENCE 797 AA; 89924 MW; CF1D5F21EEEA5691 CRC64;

Query Match      32.6%; Score 1600; DB 13; Length 797;
Best Local Similarity 43.0%; Pred. No. 2.8e-102;
Matches 379; Conservative 105; Mismatches 220; Indels 178; Gaps 27;

QY 112 LDEBQ-----PSQPS-ALECHPERGCVPEPGAAVAASKGLPOOLPAPDEDDSAAP 163
DB 21 LDTELQEADSANFPMQPEARRIHFTKS-----SDSKGDSSTL-----EPDNAOE 66
QY 164 STLSILGTPFLGSSCSADLKILSEASTMOLLOQOOQEAUSEGSSSGRAEASGAPTSS 223
DB 67 NA---YGFGLSDDLHDCCTDQKSLPTAPRNREINPHSDACVNSCSEA----- 113
QY 224 KDNVLTGTSTISDNACKELKAVSYSMGLGVEALEHLSLSP-----GEQLRGDCMY-APL 274
DB 114 -----CTTISEARELCKAVSYSLGLNMDSENMENEPGHNLASSIGSLDKRKNFMEVPF 166
QY 275 LGVPPAVRPTCAPLAECKGLLDDSAKSTEDTAEYSPKGGYTKLEGE----- 325
DB 167 LG---SSGTQESVPRAEYKCARLHD--GQLLQNDLSEGMFKTHVOGLTNEVAPSHLSS 221
QY 326 -----SLGCGSAAAGSGTLE-----LPSTLSLYKSGALDEAAA 360
DB 222 YSNMDTQTRLNAETETSAKQESCMTMDAARSGFCQFDOLLPTTLAQYSQ--IDPLSM 279
QY 361 ---VQSRDYNYFPLALAGPPPPPPHPHA-----RIKENPLDY-GSAWA 402
DB 280 GRSNFRSQFFYK-TLALANEAV-----EHAEGRYVDSSIQSPKIKTENLQNGSGSW- 331
QY 403 AAAACRYGDLASLHGAAGPGSGSPSAASSSWHTLFTAEGQLYGPCYGGGGGGGG 462
DB 332 --DHQRYNE-----NWSQYGFPSRHLHPYC----- 356
QY 463 GGGGGGGGGGGGAGAVAPYGYTRPPQGLAGQESDFTAPDVWYVPGMVSRYVPSPTC 522
DB 357 -----TETNNQFVVEFDYQ---GGGLLPRBSASESWFPGMLSKMPTNLPC 403
QY 523 VKSEMGFWMDSYSGPYGDMRLFTARDHVLIDYFFPQKTYCLICGDBASCHYGALTCG 581
DB 404 LKTEVADWLEV---PCSDRMLEGGREHVFDFMEFFFPQRTCLICADEASCHYGALTCG 460
QY 582 SKCVFFKRAAEKQYLCASRNDCTIDFRKNCPCSLRKYCAGMTLGARKLKLGNL 641
DB 461 SKCVFFKRAAEKQYLCASRNDCTIDLRKNCPCSLRKYCAGMTLGARKLKLGNL 520

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